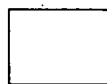


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Figure 1a



M_r (K) 1 2 3 4

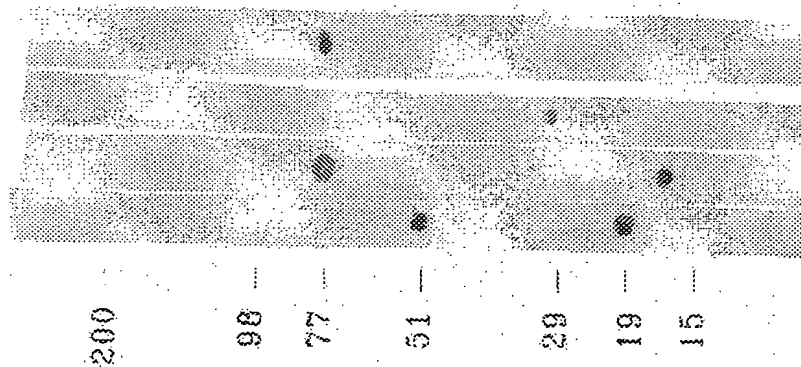
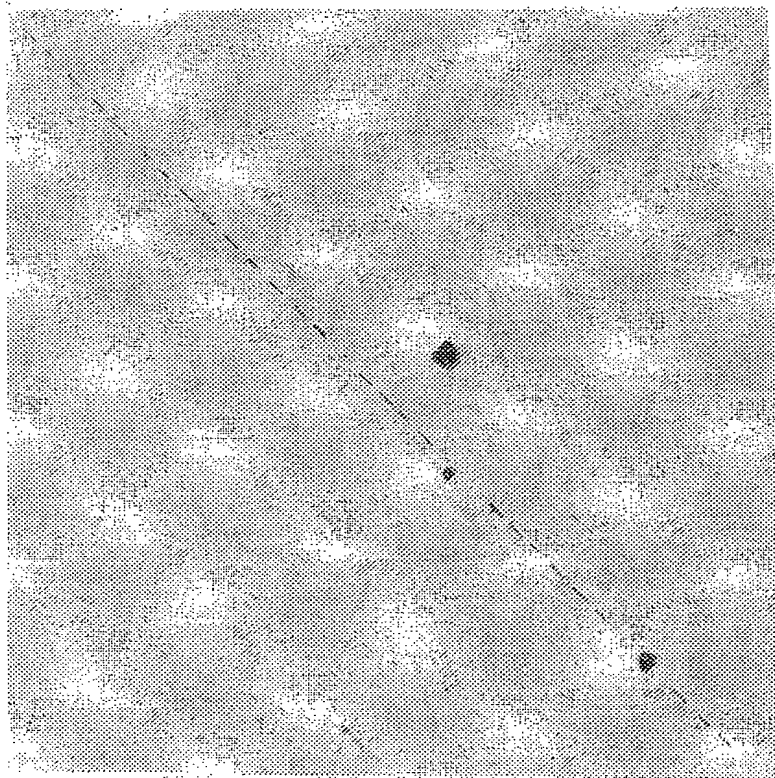


Figure 1b

← Non-reduced

15 19 29 51 77 98 200 M_r (K)



Reduced →



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Figure 2

— C1r/C1s —>

MASP-2 TPLGPKWPEPVFGRLASPGFPEYANDQERRWTLTAPPGYRLRLYFTHFDELSHLCEYDFVKLSSGAKVLATLCEQESTDTERAPGKDT 90

MASP-1 HTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFGRETDTDEQTPGQEV 87

C1r SIPIPKLFGVETSPFLFPKYPNNFETTTTITVPTGYRVKLVFQQPDLEPSEGCFYDYVKISADKKSLSGRFGQQLGSPLGNPPGKKE 87

C1s EPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGYGIHLYFTHLDIELSENCAYSVQIISGDTEEGRLCGQRSSNNPHSPIVEE 83

* * * * *

EGF —>

MASP-2 FYSLGSSLDITFRSDYSNEKP FTGFEAFYAARDIDEEO VAPGEA PTCDDHCHNHLGGFYCSERAGYVLHRNKRTCSALCS 170

MASP-1 VLSPGSFMSTITFRSDFSNEER FTGFDAYHMAVDVDEEK EREDEE LSCDHYCHNYIGGYCSERFGYILHTDNRTSERVECS 167

C1r FMSQGNKMLLTFTDFSNENGTIMFYKGLAYYQAVDLDEASRSKSGEEDPOPCQHLCHNYVGGYFCSERPGYELQEDRHSQAECS 177

C1s FQVPYNKLQVIFKSDFSNEER FTGFAAYVATDINEET DFVD VPESHFNFFIGGYFCSERPPEYFLHDDMKNGVNES 161

* * * * *

— C1r/C1s —>

MASP-2 GQVFTQSGELSSPEYPRPYKLSSTYISISLEEGFSVILDFV ESFDVET HPETLCFYPDFLKIQTDRREEHGPFGKTLPHR IETKS 256

MASP-1 DNLFTQRTGVITSPDPFPNYPYKSSSECLYTIELEEGFMVNLOFE DIFDIED HPEVPEPYDYIKIKVGPKVLGPPGGEKAPEP ISTQS 253

C1r SELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKFL EPFDIDD HQQVHEPYDQLQIYANGKNIGEFQKQRPDP LDTSS 263

C1s GDVFTALIGEIASPNYPKYPENSRCYEQIRLEKGFQVVTLRREDFDVEAADSAGN LDSLVFVAGDRQFGPYCGHGFPGPLNIETKS 250

* * * * *

CCP-1 —>

MASP-2 NTVTITFVTDESGDHTGWKIHYTSTAQPCPYPMAPPN GHVSPVQAKYILKDSFSIFMETGYELLQGHPLKSFTAVCQKDGSDWRPMPA 345

MASP-1 HSVLILFHSNDNGENRGWRLSYRAAGNEPELQPPVH GKIEPSQAKYFFKDQVLVSQDTGYKVLKDNVEMDTFQIECLKDGTWSNKIPT 342

C1r NAVDLLFTDESGDSRGWKLRYTTEIIKQPPKTLDEFTIIQNLQPYQFRDYFIATCKQGYQLIEGNQVLHSFTAVCQDDGTWHRAMPR 353

C1s NALDIIPTQDTLTGQKKGWKLRYHGDPMPCPKEDTPN SVWEPKAKYVFRDVOITCLDGFVVEGRVGTATSYSTCQSNKGWSNKLK 338

* * * * *

CCP-2 —>

MASP-2 CSIVDCGPPDDLPSGRVEYITGPGVTTYKAVIQYSCBETFYTM KVNDGKYVCEADGFWTSSKGEKSLPVECPVCGLS ARTT 426

MASP-1 CKIVDCRAPGELEHGLITFSTRNNLTYYKSEIKYSQEPYKML NNTNGIYTCQAQGVWMNKVLRSLPTCLEVGLPKFSRKL 426

C1r CKIKDCGQPRNLNPGDFRYTTTGMVNTYKARIQYCHEPYKMQTRAGSRESEQGVYTCTAQGIWNEQKGEKIPRELPGCKPVNPVEQ 443

C1s CQPVDCGIPESIENGKVE DPESTLFGSVIRYTCBEPYYME NGGGGEYHCAGNGSWVNEVLGPCLPKCPVPGVPREPPEE 419

* * * * *

serine protease —>

MASP-2 GGRIYGGQKAKPGDFPWQVLILGTTA AGALLYDNWVLTAH AVYEQKHDSALDIRMGTLRKLSPHYTQAWSEAVFIHEG 507

MASP-1 MARIFNGRPAQKGTTPWIAMLSHLNGQPPCGGSLGSSWIVTAACHLQSLDPKDPTRLRSDLLSPSD FKIIILGKHWRLSRSDENEQHLG 515

C1r RQRIIGGQKAKMGNFPWQVFTNIHGRG GGALLGDRWILTAH TLYPKEHEAQSNASLDVFLGHTNVHEELMKLGNHP IRRV 523

C1s KQRIIGGSADIKNFPWQVFFDNPA GGALINEYWVLTAH VVEGNREPTMYVGSTSVQTSRLAKSKMLT PEHVFIHPG 498

* * * * *

YTHDAG

MASP-2 YTHDAG FDNIDIALIKLNNKVINSNITPICLPRKEAESFMRTDDIGTASGWGLTQRGFLARNLMYVDIPIVDHQAATAAYEK 589

MASP-1 VKHTTLHPKYDPNTFENDVALVELLESPLNAPVMPICLP EGPOQEGAMVIVSGWGKQLQRFPELMEIEIPIVDHSTQOKAY 599

C1r SVHPDYRQDESYN PEGDIALLELENSVTLPNLLPICLP DNDTFYDLGLMGYVSGFGVMEEK IAHDLRFVRLPVPANPQAGEN WLR 608

C1s WKLLV PEGRTN FDNIDIALVRLKDPVKMGPTVSPICLPGTSSDYNLMDGLGISGWRTEKRDRAVRLKAARLPVAPLRKKEVKVE 586

* * * * *

PPYPRG

MASP-2 PPYPRG SVTANMLCAGLES GGKDSERGDSSGALVFLDS ETERWFVGGIVSWGSMNCGEAGQYGVYTKVINYIPWIENIISDF 671

MASP-1 APLKK KVTRDMICAGEKEGGKDAESGDSGGPMVTLNR ERGQWYLVGTVSWG DCGKKDRYGVVSYIHHNKDWIQRVTGVNR 680

C1r GKNRMD VFSQNMFCAGHPSLKQDAQCGDSGGVFAVRDP NTRDWATGIVSWG GCSRG YGFYTKVLNVYDVIKKEMEED 688

C1s KPTADAEAYVFTPNMICAGGEK GMDSCKGDSGGAFVQDPNDKTFYAGLVSWG QCGT YGLYTRVQNVYDVIKMTMQENSTPRED 673

* * * * *

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Figure 3a

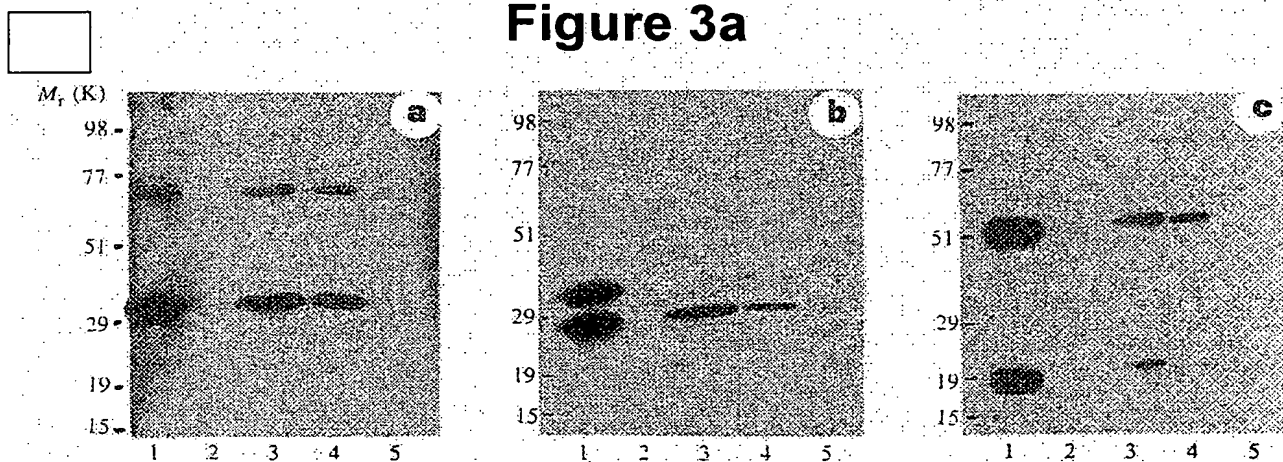
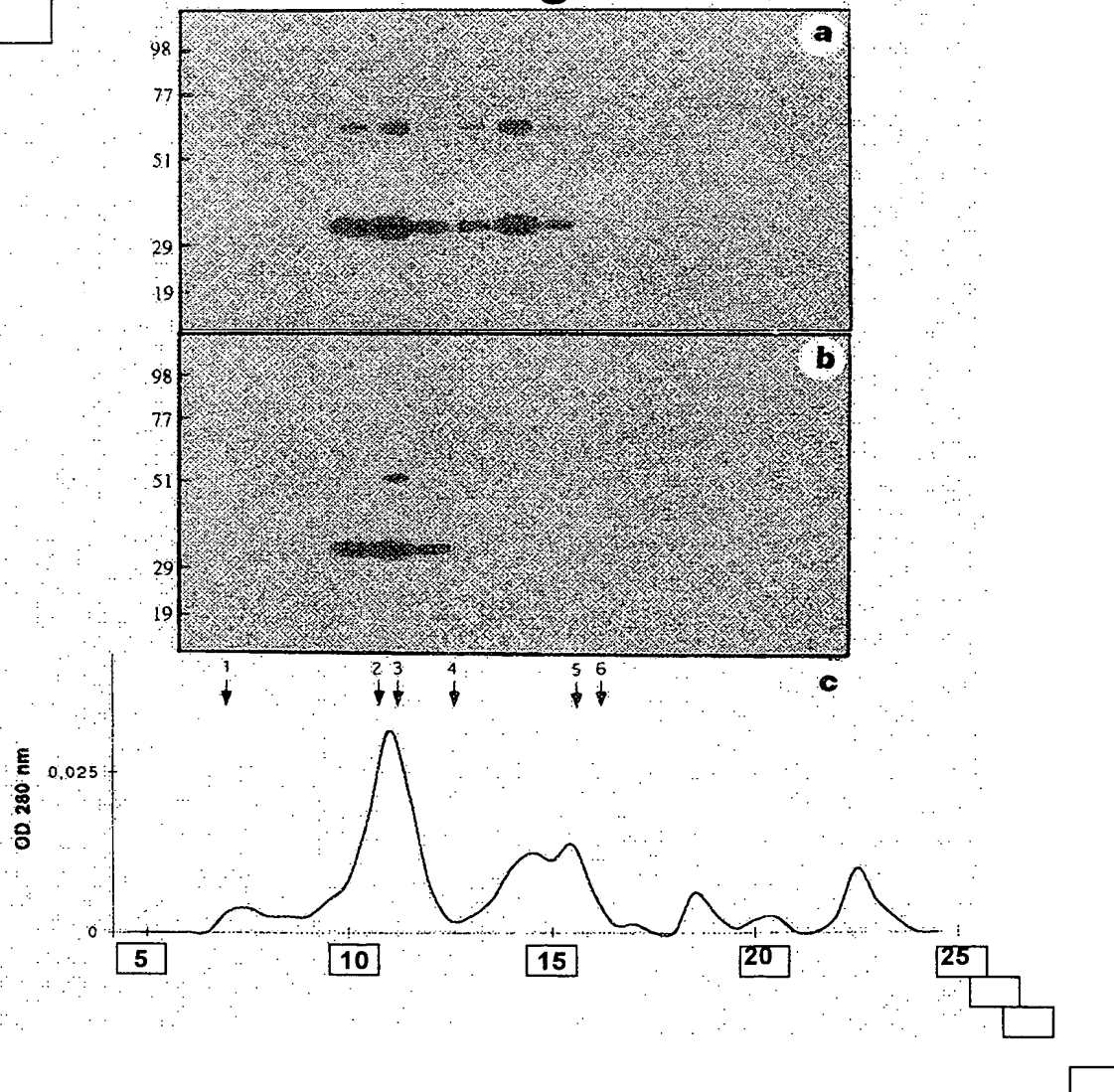
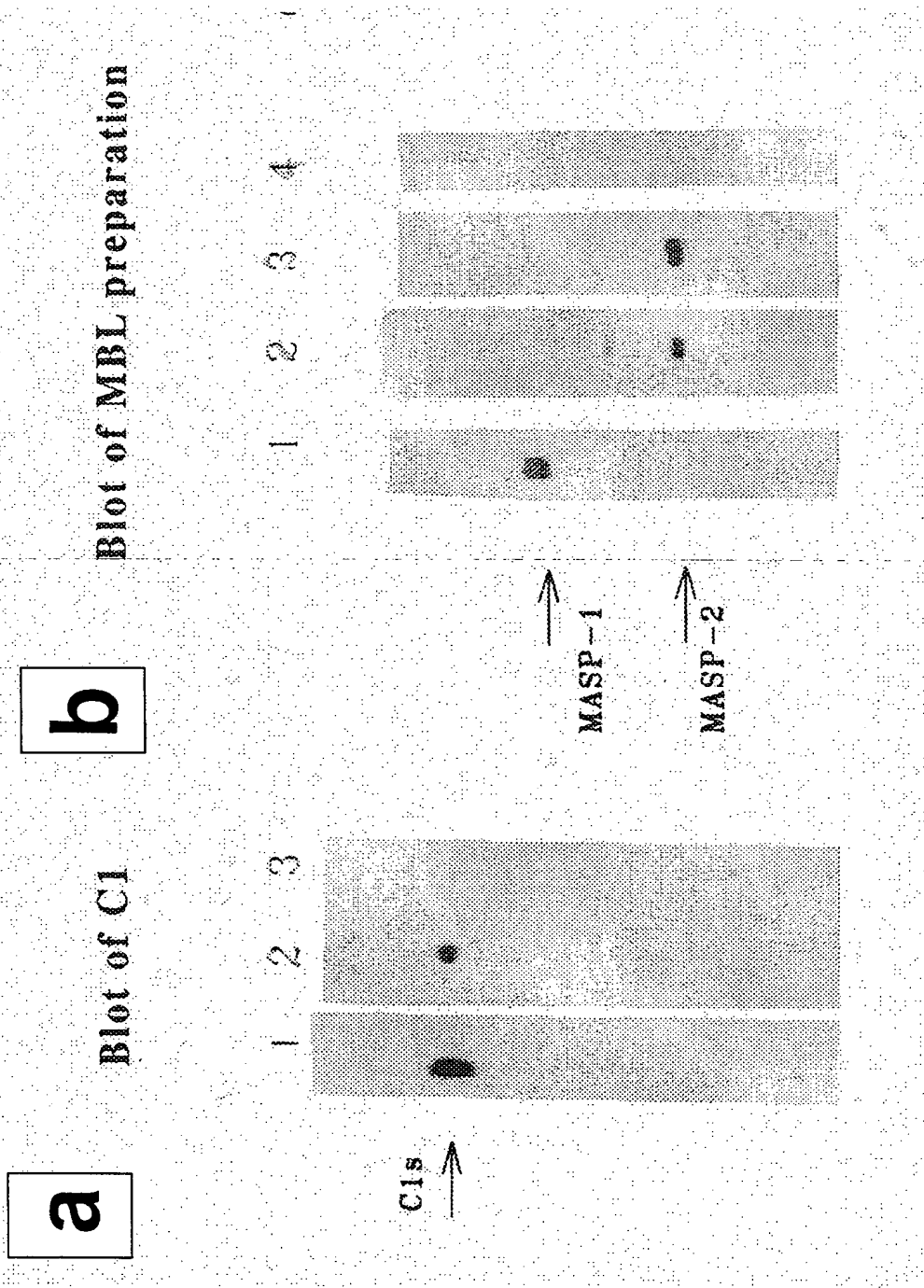


Figure 3b



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Figure 4



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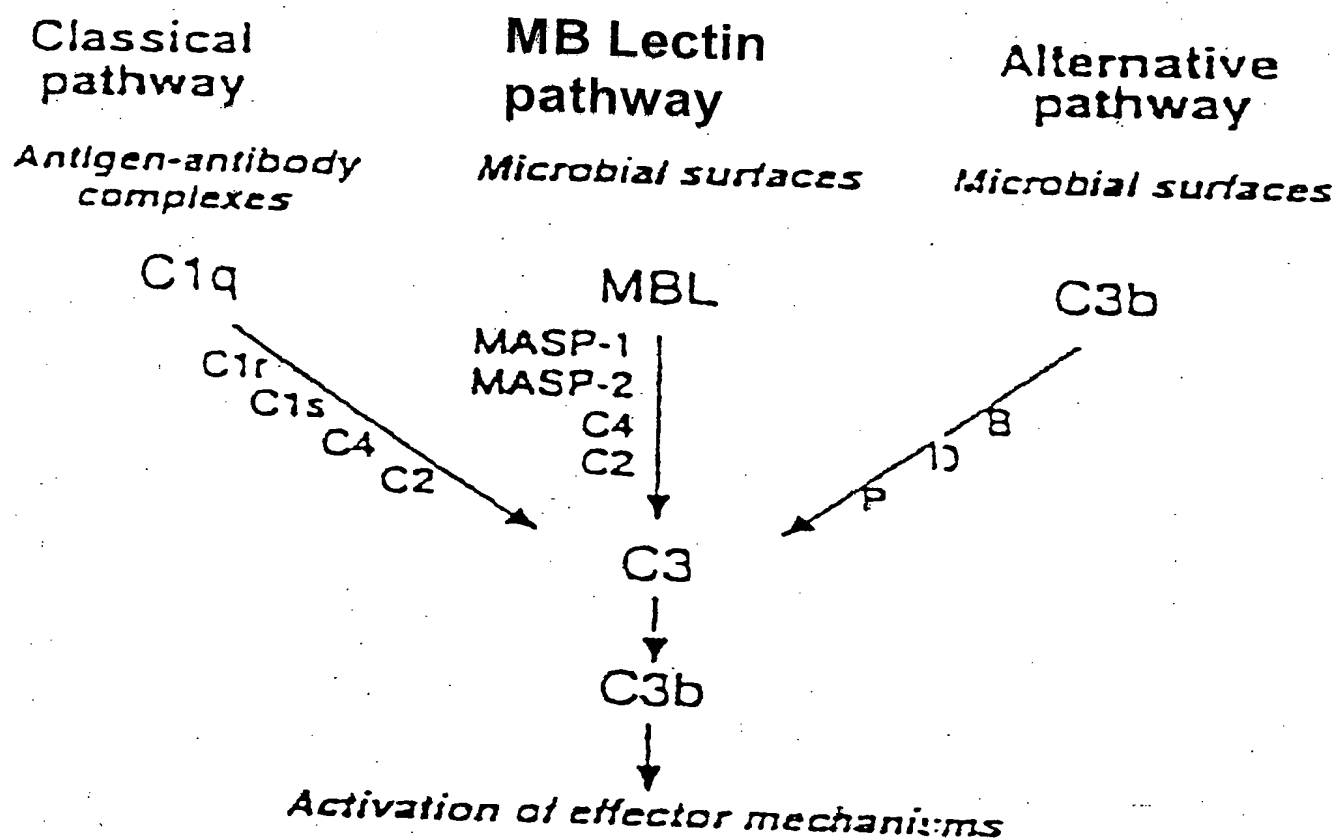


Figure 5



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Figure 6